

APRIL/MAY 2025

23PEMB24A — BIOINFORMATICS

Time : Three hours

Maximum : 75 marks

SECTION A — (10 × 2 = 20 marks)

Answer ALL the questions.

1. Define cluster analysis.
2. What are biological databases?
3. Find out the ultrametric trees.
4. Tell about substitution matrix.
5. Illustrate the 3D prediction of protein.
6. Homology modelling.
7. Short explain about Biojava.
8. Label the computational biology.
9. Simplify the Rigid Docking.
10. Outlines of Genomics.



SECTION B — (5 × 5 = 25 marks)

Answer ALL the questions.

11. (a) List out the biological data management.

Or

- (b) Organize the function biological algorithms.

12. (a) Discuss about the concept of dendrograms.

Or

- (b) How to reconstruct trees from additive matrix?

13. (a) Show about the Homology modelling.

Or

- (b) Examine the prediction of protein's function from structure.

14. (a) Construct the 3D autocorrelation.

Or

- (b) Distinguish about the prediction of the toxicity of compounds.

15. (a) Categorize the molecular docking software.

Or

- (b) Analyse the subtractive genomics.

SECTION C — (3 × 10 = 30 marks)

Answer any THREE questions.

16. Extend information of biological data mining.

17. Compile the construction of phylogenetic tree.

18. Determine the computational protein structure prediction.

19. Estimate the prediction property of Ligand compounds.

20. Recommend the principles of Immunoinformatics and vaccine development.

